

Serial Number: 09/700,687

CRF Processing Date: \_\_\_\_\_  
 Edited by: \_\_\_\_\_  
 Verified by: \_\_\_\_\_ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;  
☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Edited a format error in the <110> Applicant data section.

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

PCT

## RAW SEQUENCE LISTING

DATE: 04/04/2001

PATENT APPLICATION: US/09/700,687

TIME: 11:43:18

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

W--> 3 <110> COMPAGNIE GERVAIS DANONE  
W--> 4 GENDRE, Francois  
W--> 5 BENBADIS, Laurent  
W--> 6 BRIGNON, Pierre  
W--> 0 <110> APPLICANT:  
8 <120> TITLE OF INVENTION: MUTANT LACTOBACILLUS BULGARICUS STRAINS FREE  
9 FROM BETA-GALACTOSIDASE ACTIVITY  
11 <130> FILE REFERENCE: MJPcb191/143  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/700,687  
C--> 14 <141> CURRENT FILING DATE: 2000-11-17  
16 <150> PRIOR APPLICATION NUMBER: FR9806456  
17 <151> PRIOR FILING DATE: 1998-05-22  
19 <160> NUMBER OF SEQ ID NOS: 3  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 5059  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Lactobacillus bulgaricus  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (122)..(1873)  
32 <220> FEATURE:  
33 <221> NAME/KEY: CDS  
34 <222> LOCATION: (1877)..(4519)  
36 <400> SEQUENCE: 1  
37 gcttgtctca cgcttgcgt acgcggccgg tgcctttggc aacgacgtct tctacgcgac 60  
39 tctgtcaacc tactttatcg tcttgcac caccacctc tttaatgcg gtgaccacaa 120  
41 g atg atc ttt atc atc acc aac ttg atc acc gcc atc cgg atc ggg gaa 169  
42 Met Ile Phe Ile Ile Thr Asn Leu Ile Thr Ala Ile Arg Ile Gly Glu  
43 1 5 10 15  
45 gtc ctg ctc gac ccc ttg atc ggt aac gcc atc gac cgg acc gaa agc 217  
46 Val Leu Leu Asp Pro Leu Ile Gly Asn Ala Ile Asp Arg Thr Glu Ser  
47 20 25 30  
49 cgg tgg ggg aag ttc aag ccc tgg gtt gtg ggc ggg ggg atc atc agc 265  
50 Arg Trp Gly Lys Phe Lys Pro Trp Val Val Gly Gly Gly Ile Ile Ser  
51 35 40 45  
53 tca tta gcc ctc tta gcc ctc ttt acc gac ttt ggc ggc att aac caa 313  
54 Ser Leu Ala Leu Leu Ala Leu Phe Thr Asp Phe Gly Gly Ile Asn Gln  
55 50 55 60  
57 agc aac ccc gtt gtt tac tta gta atc ttc ggt att gtt tac ttg att 361  
58 Ser Asn Pro Val Val Tyr Leu Val Ile Phe Gly Ile Val Tyr Leu Ile  
59 65 70 75 80  
61 atg gat atc ttc tac tca ttt aaa gac act ggc ttc tgg gcc atg atc 409  
62 Met Asp Ile Phe Tyr Ser Phe Lys Asp Thr Gly Phe Trp Ala Met Ile  
63 85 90 95  
65 ccg gcc ttg tcc ctg gat tcc cgg gaa aga gag aag acc tcc acc ttc 457  
66 Pro Ala Leu Ser Leu Asp Ser Arg Glu Arg Glu Lys Thr Ser Thr Phe

*Format errors in  
<110> Applicant data section.*

*Does Not Comply  
Corrected Diskette Needed*

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Input Set : A:\PTO.txt

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67	100	105	110	
69 gcc aga gtc ggc tcc acc atc ggg gcc aac ctg gtc ggg gta gtc atc	505			
70 Ala Arg Val Gly Ser Thr Ile Gly Ala Asn Leu Val Gly Val Val Ile				
71 115 120 125				
73 acc cca atc atc ctc ttc ttc tcg gcc agc aag gcc aac ccc aac ggg	553			
74 Thr Pro Ile Ile Leu Phe Phe Ser Ala Ser Lys Ala Asn Pro Asn Gly				
75 130 135 140				
77 gat aag cag ggc tgg ttc ttc ttt gcc ttg atc gtg gcc att gtc ggc	601			
78 Asp Lys Gln Gly Trp Phe Phe Phe Ala Leu Ile Val Ala Ile Val Gly				
79 145 150 155 160				
81 atc ttg acc tca att acc gtt ggt ctt ggt act cac gaa gta aaa tcc	649			
82 Ile Leu Thr Ser Ile Thr Val Gly Leu Gly Thr His Glu Val Lys Ser				
83 165 170 175				
85 gcc ctg cgg gaa agc aat gaa aag acc act ttg aag cag gtc ttt aag	697			
86 Ala Leu Arg Glu Ser Asn Glu Lys Thr Thr Leu Lys Gln Val Phe Lys				
87 180 185 190				
89 gtc ctg ggg caa aac gac cag ctc ctc tgg ctg gcc ttt gcc tac tgg	745			
90 Val Leu Gly Gln Asn Asp Gln Leu Trp Leu Ala Phe Ala Tyr Trp				
91 195 200 205				
93 ttt tac ggc ctg ggt atc aac acc ctg aac gct ctg caa ctt tac tac	793			
94 Phe Tyr Gly Leu Gly Ile Asn Thr Leu Asn Ala Leu Gln Leu Tyr Tyr				
95 210 215 220				
97 ttc tca tac atc tta ggc gat gcc cgc ggc tac agc ctg ctt tac acc	841			
98 Phe Ser Tyr Ile Leu Gly Asp Ala Arg Gly Tyr Ser Leu Leu Tyr Thr				
99 225 230 235 240				
101 atc aac acc ttt gtc ggt tta atc tct gca tcc ttc ttc cca tca ctg	889			
102 Ile Asn Thr Phe Val Gly Leu Ile Ser Ala Ser Phe Phe Pro Ser Leu				
103 245 250 255				
105 gcc aag aag ttc aac aga aat cgc ctc ttc tac gcc tgc atc gcg gtg	937			
106 Ala Lys Lys Phe Asn Arg Asn Arg Leu Phe Tyr Ala Cys Ile Ala Val				
107 260 265 270				
109 atg ctg tta ggg atc ggg gtc ttc tcc gtg gcc agc ggt tct ctg gcc	985			
110 Met Leu Leu Gly Ile Gly Val Phe Ser Val Ala Ser Gly Ser Leu Ala				
111 275 280 285				
113 ctg tcc ctt gtt ggg gca gaa ttc ttc ttt att ccg cag cct ctg gcc	1033			
114 Leu Ser Leu Val Gly Ala Glu Phe Phe Phe Ile Pro Gln Pro Leu Ala				
115 290 295 300				
117 ttc ctg gtc gtt ttg atg atc atc tct gac gct gtt gaa tac ggc cag	1081			
118 Phe Leu Val Val Leu Met Ile Ile Ser Asp Ala Val Glu Tyr Gly Gln				
119 305 310 315 320				
121 ctg aaa act ggc cac aga gac gaa gct ttg acc ctg tct gtc cgg cca	1129			
122 Leu Lys Thr Gly His Arg Asp Glu Ala Leu Thr Leu Ser Val Arg Pro				
123 325 330 335				
125 ttg gtc gat aag ctg ggc ggg gcc ttg tcc aac tgg ttt gtt tcc ttg	1177			
126 Leu Val Asp Lys Leu Gly Gly Ala Leu Ser Asn Trp Phe Val Ser Leu				
127 340 345 350				
129 att gcc tta act gcc ggc atg acc act ggg gcg act gcc tca aca att	1225			
130 Ile Ala Leu Thr Ala Gly Met Thr Thr Gly Ala Thr Ala Ser Thr Ile				
131 355 360 365				

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133	aca	gct	cat	ggc	cag	atg	gtc	ttc	aag	tta	gct	atg	ttt	gcc	tta	ccg	1273
134	Thr	Ala	His	Gly	Gln	Met	Val	Phe	Lys	Leu	Ala	Met	Phe	Ala	Leu	Pro	
135		370					375					380					
137	gca	gtc	atg	ctc	ttg	atc	gct	gtt	tct	att	ttc	gcc	aaa	aag	gtc	ttc	1321
138	Ala	Val	Met	Leu	Leu	Ile	Ala	Val	Ser	Ile	Phe	Ala	Lys	Lys	Val	Phe	
139	385					390					395				400		
141	ttg	act	gaa	gaa	aag	cac	gcg	gaa	atc	gtc	gac	cag	ctg	gaa	act	caa	1369
142	Leu	Thr	Glu	Glu	Lys	His	Ala	Glu	Ile	Val	Asp	Gln	Leu	Glu	Thr	Gln	
143					405					410					415		
145	ttc	agc	caa	agc	cat	gcc	caa	aag	ccg	gcg	caa	gct	gaa	agc	ttc	act	1417
146	Phe	Ser	Gln	Ser	His	Ala	Gln	Lys	Pro	Ala	Gln	Ala	Glu	Ser	Phe	Thr	
147				420					425						430		
149	ttg	gcc	agc	cca	gtc	tcc	gga	caa	tta	atg	aac	ctg	gac	atg	gtt	gac	1465
150	Leu	Ala	Ser	Pro	Val	Ser	Gly	Gln	Leu	Met	Asn	Leu	Asp	Met	Val	Asp	
151			435				440						445				
153	gac	ccg	gtc	ttt	gcc	gac	aaa	aag	tta	ggc	gac	ggc	ttt	gcc	ctg	gtg	1513
154	Asp	Pro	Val	Phe	Ala	Asp	Lys	Lys	Leu	Gly	Asp	Gly	Phe	Ala	Leu	Val	
155		450					455						460				
157	cca	gca	gac	ggt	aag	gtc	tac	gcg	cca	ttt	gcc	ggt	act	gtc	cg	cag	1561
158	Pro	Ala	Asp	Gly	Lys	Val	Tyr	Ala	Pro	Phe	Ala	Gly	Thr	Val	Arg	Gln	
159	465				470					475					480		
161	ctg	gcc	aag	acc	cg	cac	tcg	atc	gtc	ctg	gaa	aat	gaa	cat	ggg	gtc	1609
162	Leu	Ala	Lys	Thr	Arg	His	Ser	Ile	Val	Leu	Glu	Asn	Glu	His	Gly	Val	
163				485					490						495		
165	ttg	gtc	ttg	att	cac	ctt	ggc	ctg	ggc	acg	gtc	aaa	tta	aac	ggg	act	1657
166	Leu	Val	Leu	Ile	His	Leu	Gly	Leu	Gly	Thr	Val	Lys	Leu	Asn	Gly	Thr	
167			500						505						510		
169	ggc	ttt	gtc	agc	tat	gtt	gaa	gag	ggc	agc	cag	gta	gaa	gcc	ggc	cag	1705
170	Gly	Phe	Val	Ser	Tyr	Val	Glu	Glu	Gly	Ser	Gln	Val	Glu	Ala	Gly	Gln	
171		515							520						525		
173	cag	atc	ctg	gaa	ttc	tgg	gac	ccg	gcg	atc	aag	cag	gcc	aag	ctg	gac	1753
174	Gln	Ile	Leu	Glu	Phe	Trp	Asp	Pro	Ala	Ile	Lys	Gln	Ala	Lys	Leu	Asp	
175		530					535						540				
177	gac	acg	gta	atc	gtg	acc	gtc	atc	aac	agc	gaa	act	ttc	gca	aat	agc	1801
178	Asp	Thr	Val	Ile	Val	Thr	Val	Ile	Asn	Ser	Glu	Thr	Phe	Ala	Asn	Ser	
179	545					550					555					560	
181	cag	atg	ctc	ttg	ccg	atc	ggc	cac	agc	gtc	caa	gcc	ctg	gat	gat	gta	1849
182	Gln	Met	Leu	Leu	Pro	Ile	Gly	His	Ser	Val	Gln	Ala	Leu	Asp	Asp	Val	
183				565						570					575		
185	ttc	aag	tta	gaa	ggg	aag	aat	tag	aaa	atg	agc	aat	aag	tta	gta	aaa	1897
186	Phe	Lys	Leu	Glu	Gly	Lys	Asn			Met	Ser	Asn	Lys	Leu	Val	Lys	
W--> 187			580							585					590		
189	gaa	aaa	aga	gtt	gac	cag	gca	gac	ttg	gcc	tgg	ctg	act	gac	ccg	gaa	1945
190	Glu	Lys	Arg	Val	Asp	Gln	Ala	Asp	Leu	Ala	Trp	Leu	Thr	Asp	Pro	Glu	
W--> 191			595						600					605			
193	gtt	tac	gaa	gtc	aat	aca	att	ccc	ccg	cac	tcc	gac	cat	gag	tcc	ttc	1993
194	Val	Tyr	Glu	Val	Asn	Thr	Ile	Pro	Pro	His	Ser	Asp	His	Glu	Ser	Phe	
W--> 195			610					615						620			
197	caa	agc	cag	gaa	gaa	ctg	gag	gag	ggc	aag	tcc	agt	tta	gtg	cag	tcc	2041

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Input Set : A:\PTO.txt

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198 Gln Ser Gln Glu Glu Leu Glu Glu Gly Lys Ser Ser Leu Val Gln Ser
W--> 199      625      630      635
201 ctg gac ggg gac tgg ctg att gac tac gct gaa aac ggc cag gga cca 2089
202 Leu Asp Gly Asp Trp Leu Ile Asp Tyr Ala Glu Asn Gly Gln Gly Pro
W--> 203 640      645      650      655
205 gtc aac ttc tat gca gaa gac ttt gac gat agc aat ttt aag tca gtc 2137
206 Val Asn Phe Tyr Ala Glu Asp Phe Asp Asp Ser Asn Phe Lys Ser Val
W--> 207      660      665      670
209 aaa gta ccc ggc aac ctg gaa ctg caa ggc ttt ggc cag ccc cag tat 2185
210 Lys Val Pro Gly Asn Leu Glu Leu Gln Gly Phe Gly Gln Pro Gln Tyr
W--> 211      675      680      685
213 gtc aac gtc caa tat cca tgg gac ggc agt gag gag att ttc ccg ccc 2233
214 Val Asn Val Gln Tyr Pro Trp Asp Gly Ser Glu Glu Ile Phe Pro Pro
W--> 215      690      695      700
217 caa att cca agc aaa aat ccg ctc gct tct tat gtc aga tac ttt gac 2281
218 Gln Ile Pro Ser Lys Asn Pro Leu Ala Ser Tyr Val Arg Tyr Phe Asp
W--> 219      705      710      715
221 ctg gat gaa gct ttc tgg gac aag gaa gtc agc ttg aag ttt gac ggg 2329
222 Leu Asp Glu Ala Phe Trp Asp Lys Glu Val Ser Leu Lys Phe Asp Gly
W--> 223 720      725      730      735
225 gcg gca aca gcc atc tat gtc tgg ctg aac ggc cac ttc gtc ggc tac 2377
226 Ala Ala Thr Ala Ile Tyr Val Trp Leu Asn Gly His Phe Val Gly Tyr
W--> 227      740      745      750
229 ggg gaa gac tcc ttt acc cca agc gag ttt atg gtt acc aag ttc ctc 2425
230 Gly Glu Asp Ser Phe Thr Pro Ser Glu Phe Met Val Thr Lys Phe Leu
W--> 231      755      760      765
233 aag aaa gaa aat aac cgc ctg gca gtg gct ctc tac aag tat tct tcc 2473
234 Lys Lys Glu Asn Asn Arg Leu Ala Val Ala Leu Tyr Lys Tyr Ser Ser
W--> 235      770      775      780
237 gcc tcc tgg ctg gaa gac cag gac ttc tgg cgc atg tct ggt ttg ttc 2521
238 Ala Ser Trp Leu Glu Asp Gln Asp Phe Trp Arg Met Ser Gly Leu Phe
W--> 239      785      790      795
241 aga tca gtg act ctt cag gcc aag ccg cgt ctg cac ttg gag gac ctt 2569
242 Arg Ser Val Thr Leu Gln Ala Lys Pro Arg Leu His Leu Glu Asp Leu
W--> 243 800      805      810      815
245 aag ctt acg gcc agc ttg acc gat aac tac caa aaa gga aag ctg gaa 2617
246 Lys Leu Thr Ala Ser Leu Thr Asp Asn Tyr Gln Lys Gly Lys Leu Glu
W--> 247      820      825      830
249 gtc gaa gcc aat att gcc tac cgc ttg cca aat gcc agc ttt aag ctg 2665
250 Val Glu Ala Asn Ile Ala Tyr Arg Leu Pro Asn Ala Ser Phe Lys Leu
W--> 251      835      840      845
253 gaa gtg cgg gat agt gaa ggt gac ttg gtt gct gaa aag ctg ggc cca 2713
254 Glu Val Arg Asp Ser Glu Gly Asp Leu Val Ala Glu Lys Leu Gly Pro
W--> 255      850      855      860
257 atc aga agc gag cag ctg gaa ttc act ctg gct gat ttg cca gta gct 2761
258 Ile Arg Ser Glu Gln Leu Glu Phe Thr Leu Ala Asp Leu Pro Val Ala
W--> 259      865      870      875
261 gcc tgg agc gcg gaa aag cct aac ctt tac cag gtc cgc ctg tat tta 2809
262 Ala Trp Ser Ala Glu Lys Pro Asn Leu Tyr Gln Val Arg Leu Tyr Leu

```

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```

W--> 263 880                885                890                895
      265 tac cag gca ggc agc ctc tta gag gtt agc cgg cag gaa gtg ggt ttc 2857
      266 Tyr Gln Ala Gly Ser Leu Leu Glu Val Ser Arg Gln Glu Val Gly Phe
W--> 267                900                905                910
      269 cgc aac ttt gaa cta aaa gac ggg att atg tac ctt aac ggc cag cgg 2905
      270 Arg Asn Phe Glu Leu Lys Asp Gly Ile Met Tyr Leu Asn Gly Gln Arg
W--> 271                915                920                925
      273 atc gtc ttc aag ggg gcc aac cgg cac gaa ttt gac agt aag ttg ggc 2953
      274 Ile Val Phe Lys Gly Ala Asn Arg His Glu Phe Asp Ser Lys Leu Gly
W--> 275                930                935                940
      277 cgg gct atc aca gaa gag gat atg atc tgg gat atc aag acc atg aag 3001
      278 Arg Ala Ile Thr Glu Glu Asp Met Ile Trp Asp Ile Lys Thr Met Lys
W--> 279                945                950                955
      281 cga agc aac atc aat gct gtc cgc tgc tct cac tac ccg aac cag tcc 3049
      282 Arg Ser Asn Ile Asn Ala Val Arg Cys Ser His Tyr Pro Asn Gln Ser
W--> 283 960                965                970                975
      285 ctc ttt tac cgg ctc tgt gac aag tac ggc ctt tac gtc att gat gaa 3097
      286 Leu Phe Tyr Arg Leu Cys Asp Lys Tyr Gly Leu Tyr Val Ile Asp Glu
W--> 287                980                985                990
      289 gct aac ctg gaa agc cac ggc acc tgg gaa aaa gtg ggg ggg cac gaa 3145
      290 Ala Asn Leu Glu Ser His Gly Thr Trp Glu Lys Val Gly Gly His Glu
W--> 291                995                1000                1005
      293 gat cct agc ttc aat gtt cca ggc gat gac cag cat tgg ctg gga gcc 3193
      294 Asp Pro Ser Phe Asn Val Pro Gly Asp Asp Gln His Trp Leu Gly Ala
W--> 295                1010                1015                1020
      297 agc tta tcc cgg gtg aag aac atg atg gct cgg gac aag aac cat gct 3241
      298 Ser Leu Ser Arg Val Lys Asn Met Met Ala Arg Asp Lys Asn His Ala
W--> 299                1025                1030                1035
      301 tca atc ctg atc tgg tct tta ggc aat gag tct tac gcc ggc act gtc 3289
      302 Ser Ile Leu Ile Trp Ser Leu Gly Asn Glu Ser Tyr Ala Gly Thr Val
W--> 303 1040                1045                1050                1055
      305 ttt gcc caa atg gct gat tac gtc cgg aag gct gat ccg acc cgg gtt 3337
      306 Phe Ala Gln Met Ala Asp Tyr Val Arg Lys Ala Asp Pro Thr Arg Val
W--> 307                1060                1065                1070
      309 cag cac tat gaa ggg gtg acc cac aac cgg aag ttt gac gac gcc acc 3385
      310 Gln His Tyr Glu Gly Val Thr His Asn Arg Lys Phe Asp Asp Ala Thr
W--> 311                1075                1080                1085
      313 cag att gaa agc cgg atg tat gct ccg gcc aag gta att gaa gaa tac 3433
      314 Gln Ile Glu Ser Arg Met Tyr Ala Pro Ala Lys Val Ile Glu Glu Tyr
W--> 315                1090                1095                1100
      317 ttg acc aat aaa cca gcc aag cca ttt atc tca gtt gaa tac gct cac 3481
      318 Leu Thr Asn Lys Pro Ala Lys Pro Phe Ile Ser Val Glu Tyr Ala His
W--> 319                1105                1110                1115
      321 gcc atg ggc aac tcc gtc ggt gac ctg gcc gcc tac acg gcc ctg gaa 3529
      322 Ala Met Gly Asn Ser Val Gly Asp Leu Ala Ala Tyr Thr Ala Leu Glu
W--> 323 1120                1125                1130                1135
      325 aaa tac ccc cac tac cag ggc ggc ttc atc tgg gac tgg att gac caa 3577
      326 Lys Tyr Pro His Tyr Gln Gly Gly Phe Ile Trp Asp Trp Ile Asp Gln
W--> 327                1140                1145                1150

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## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/700,687

DATE: 04/04/2001

TIME: 11:43:19

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

L:3 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:4 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:5 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:6 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:0 M:201 W: Mandatory field data missing, APPLICANT:  
L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:187 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:195 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:199 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:207 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:211 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:219 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:223 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:227 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:231 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:235 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:239 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:243 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:247 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:251 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:255 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:263 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:271 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:275 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:279 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:283 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:287 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:347 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

**VERIFICATION SUMMARY**

DATE: 04/04/2001

PATENT APPLICATION: US/09/700,687

TIME: 11:43:19

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04042001\I700687.raw

L:351 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:355 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:359 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:363 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:367 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:371 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:375 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:379 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:383 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1



PCT09

## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

```

2 <110> APPLICANT: GENDRE, Francois
3   BENBADIS, Laurent
4   BRIGNON, Pierre
5   COMPAGNIE GERVAIS DANONE
7 <120> TITLE OF INVENTION: MUTANT LACTOBACILLUS BULGARICUS STRAINS FREE
8   FROM BETA-GALACTOSIDASE ACTIVITY
10 <130> FILE REFERENCE: MJPCbl91/143
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/700,687
C--> 13 <141> CURRENT FILING DATE: 2000-11-17
15 <150> PRIOR APPLICATION NUMBER: FR9806456
16 <151> PRIOR FILING DATE: 1998-05-22
18 <160> NUMBER OF SEQ ID NOS: 3
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 5059
24 <212> TYPE: DNA
25 <213> ORGANISM: Lactobacillus bulgaricus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (122)..(1873)
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (1877)..(4519)
35 <400> SEQUENCE: 1
36 gcttgtctca cgcttgtcgt acgcgggccgg tgcctttggc aacgacgtct tctacgcgac 60
38 tctgtcaacc tactttatcg tcttcgtcac caccacctc ttaaatgccg gtgaccacaa 120
40 g atg atc ttt atc atc acc aac ttg atc acc gcc atc cgg atc ggg gaa 169
41 Met Ile Phe Ile Ile Thr Asn Leu Ile Thr Ala Ile Arg Ile Gly Glu
42 1 5 10 15
44 gtc ctg ctg gac ccc ttg atc ggt aac gcc atc gac cgg acc gaa agc 217
45 Val Leu Leu Asp Pro Leu Ile Gly Asn Ala Ile Asp Arg Thr Glu Ser
46 20 25 30
48 cgg tgg ggg aag ttc aag ccc tgg gtt gtg ggc ggg ggg atc atc agc 265
49 Arg Trp Gly Lys Phe Lys Pro Trp Val Val Gly Gly Gly Ile Ile Ser
50 35 40 45
52 tca tta gcc ctg tta gcc ctg ttt acc gac ttt ggc ggc att aac caa 313
53 Ser Leu Ala Leu Leu Ala Leu Phe Thr Asp Phe Gly Gly Ile Asn Gln
54 50 55 60
56 agc aac ccc gtt gtt tac tta gta atc ttc ggt att gtt tac ttg att 361
57 Ser Asn Pro Val Val Tyr Leu Val Ile Phe Gly Ile Val Tyr Leu Ile
58 65 70 75 80
60 atg gat atc ttc tac tca ttt aaa gac act ggc ttc tgg gcc atg atc 409
61 Met Asp Ile Phe Tyr Ser Phe Lys Asp Thr Gly Phe Trp Ala Met Ile
62 85 90 95
64 ccg gcc ttg tcc ctg gat tcc cgg gaa aga gag aag acc tcc acc ttc 457
65 Pro Ala Leu Ser Leu Asp Ser Arg Glu Arg Glu Lys Thr Ser Thr Phe
66 100 105 110

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## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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68 gcc aga gtc ggc tcc acc atc ggg gcc aac ctg gtc ggg gta gtc atc 505
69 Ala Arg Val Gly Ser Thr Ile Gly Ala Asn Leu Val Gly Val Val Ile
70      115      120      125
72 acc cca atc atc ctc ttc ttc tcg gcc agc aag gcc aac ccc aac ggg 553
73 Thr Pro Ile Ile Leu Phe Phe Ser Ala Ser Lys Ala Asn Pro Asn Gly
74      130      135      140
76 gat aag cag ggc tgg ttc ttc ttt gcc ttg atc gtg gcc att gtc ggc 601
77 Asp Lys Gln Gly Trp Phe Phe Ala Leu Ile Val Ala Ile Val Gly
78 145      150      155      160
80 atc ttg acc tca att acc gtt ggt ctt ggt act cac gaa gta aaa tcc 649
81 Ile Leu Thr Ser Ile Thr Val Gly Leu Gly Thr His Glu Val Lys Ser
82      165      170      175
84 gcc ctg cgg gaa agc aat gaa aag acc act ttg aag cag gtc ttt aag 697
85 Ala Leu Arg Glu Ser Asn Glu Lys Thr Thr Leu Lys Gln Val Phe Lys
86      180      185      190
88 gtc ctg ggg caa aac gac cag ctc ctc tgg ctg gcc ttt gcc tac tgg 745
89 Val Leu Gly Gln Asn Asp Gln Leu Leu Trp Leu Ala Phe Ala Tyr Trp
90      195      200      205
92 ttt tac ggc ctg ggt atc aac acc ctg aac gct ctg caa ctt tac tac 793
93 Phe Tyr Gly Leu Gly Ile Asn Thr Leu Asn Ala Leu Gln Leu Tyr Tyr
94      210      215      220
96 ttc tca tac atc tta ggc gat gcc cgc ggc tac agc ctg ctt tac acc 841
97 Phe Ser Tyr Ile Leu Gly Asp Ala Arg Gly Tyr Ser Leu Leu Tyr Thr
98 225      230      235      240
100 atc aac acc ttt gtc ggt tta atc tct gca tcc ttc ttc cca tca ctg 889
101 Ile Asn Thr Phe Val Gly Leu Ile Ser Ala Ser Phe Phe Pro Ser Leu
102      245      250      255
104 gcc aag aag ttc aac aga aat cgc ctc ttc tac gcc tgc atc gcg gtg 937
105 Ala Lys Lys Phe Asn Arg Asn Arg Leu Phe Tyr Ala Cys Ile Ala Val
106      260      265      270
108 atg ctg tta ggg atc ggg gtc ttc tcc gtg gcc agc ggt tct ctg gcc 985
109 Met Leu Leu Gly Ile Gly Val Phe Ser Val Ala Ser Gly Ser Leu Ala
110      275      280      285
112 ctg tcc ctt gtt ggg gca gaa ttc ttc ttt att ccg cag cct ctg gcc 1033
113 Leu Ser Leu Val Gly Ala Glu Phe Phe Phe Ile Pro Gln Pro Leu Ala
114      290      295      300
116 ttc ctg gtc gtt ttg atg atc atc tct gac gct gtt gaa tac ggc cag 1081
117 Phe Leu Val Val Leu Met Ile Ile Ser Asp Ala Val Glu Tyr Gly Gln
118 305      310      315      320
120 ctg aaa act ggc cac aga gac gaa gct ttg acc ctg tct gtc cgg cca 1129
121 Leu Lys Thr Gly His Arg Asp Glu Ala Leu Thr Leu Ser Val Arg Pro
122      325      330      335
124 ttg gtc gat aag ctg ggc ggg gcc ttg tcc aac tgg ttt gtt tcc ttg 1177
125 Leu Val Asp Lys Leu Gly Gly Ala Leu Ser Asn Trp Phe Val Ser Leu
126      340      345      350
128 att gcc tta act gcc ggc atg acc act ggg gcg act gcc tca aca att 1225
129 Ile Ala Leu Thr Ala Gly Met Thr Thr Gly Ala Thr Ala Ser Thr Ile
130      355      360      365
132 aca gct cat ggc cag atg gtc ttc aag tta gct atg ttt gcc tta ccg 1273

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## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

```

133 Thr Ala His Gly Gln Met Val Phe Lys Leu Ala Met Phe Ala Leu Pro
134      370      375      380
136 gca gtc atg ctc ttg atc gct gtt tct att ttc gcc aaa aag gtc ttc 1321
137 Ala Val Met Leu Leu Ile Ala Val Ser Ile Phe Ala Lys Lys Val Phe
138 385      390      395      400
140 ttg act gaa gaa aag cac gcg gaa atc gtc gac cag ctg gaa act caa 1369
141 Leu Thr Glu Glu Lys His Ala Glu Ile Val Asp Gln Leu Glu Thr Gln
142      405      410      415
144 ttc agc caa agc cat gcc caa aag ccg gcg caa gct gaa agc ttc act 1417
145 Phe Ser Gln Ser His Ala Gln Lys Pro Ala Gln Ala Glu Ser Phe Thr
146      420      425      430
148 ttg gcc agc cca gtc tcc gga caa tta atg aac ctg gac atg gtt gac 1465
149 Leu Ala Ser Pro Val Ser Gly Gln Leu Met Asn Leu Asp Met Val Asp
150      435      440      445
152 gac ccg gtc ttt gcc gac aaa aag tta ggc gac ggc ttt gcc ctg gtg 1513
153 Asp Pro Val Phe Ala Asp Lys Lys Leu Gly Asp Gly Phe Ala Leu Val
154      450      455      460
156 cca gca gac ggt aag gtc tac gcg cca ttt gcc ggt act gtc cgc cag 1561
157 Pro Ala Asp Gly Lys Val Tyr Ala Pro Phe Ala Gly Thr Val Arg Gln
158 465      470      475      480
160 ctg gcc aag acc cgg cac tcg atc gtc ctg gaa aat gaa cat ggg gtc 1609
161 Leu Ala Lys Thr Arg His Ser Ile Val Leu Glu Asn Glu His Gly Val
162      485      490      495
164 ttg gtc ttg att cac ctt ggc ctg ggc acg gtc aaa tta aac ggg act 1657
165 Leu Val Leu Ile His Leu Gly Leu Gly Thr Val Lys Leu Asn Gly Thr
166      500      505      510
168 ggc ttt gtc agc tat gtt gaa gag ggc agc cag gta gaa gcc ggc cag 1705
169 Gly Phe Val Ser Tyr Val Glu Glu Gly Ser Gln Val Glu Ala Gly Gln
170      515      520      525
172 cag atc ctg gaa ttc tgg gac ccg gcg atc aag cag gcc aag ctg gac 1753
173 Gln Ile Leu Glu Phe Trp Asp Pro Ala Ile Lys Gln Ala Lys Leu Asp
174      530      535      540
176 gac acg gta atc gtg acc gtc atc aac agc gaa act ttc gca aat agc 1801
177 Asp Thr Val Ile Val Thr Val Ile Asn Ser Glu Thr Phe Ala Asn Ser
178 545      550      555      560
180 cag atg ctc ttg ccg atc ggc cac agc gtc caa gcc ctg gat gat gta 1849
181 Gln Met Leu Leu Pro Ile Gly His Ser Val Gln Ala Leu Asp Asp Val
182      565      570      575
184 ttc aag tta gaa ggg aag aat tag aaa atg agc aat aag tta gta aaa 1897
185 Phe Lys Leu Glu Gly Lys Asn Met Ser Asn Lys Leu Val Lys
W--> 186      580      585      590
188 gaa aaa aga gtt gac cag gca gac ttg gcc tgg ctg act gac ccg gaa 1945
189 Glu Lys Arg Val Asp Gln Ala Asp Leu Ala Trp Leu Thr Asp Pro Glu
W--> 190      595      600      605
192 gtt tac gaa gtc aat aca att ccc ccg cac tcc gac cat gag tcc ttc 1993
193 Val Tyr Glu Val Asn Thr Ile Pro Pro His Ser Asp His Glu Ser Phe
W--> 194      610      615      620
196 caa agc cag gaa gaa ctg gag gag ggc aag tcc agt tta gtg cag tcc 2041
197 Gln Ser Gln Glu Glu Leu Glu Glu Gly Lys Ser Ser Leu Val Gln Ser

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## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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W--> 198      625      630      635
      200 ctg gac ggg gac tgg ctg att gac tac gct gaa aac ggc cag gga cca 2089
      201 Leu Asp Gly Asp Trp Leu Ile Asp Tyr Ala Glu Asn Gly Gln Gly Pro
W--> 202 640      645      650      655
      204 gtc aac ttc tat gca gaa gac ttt gac gat agc aat ttt aag tca gtc 2137
      205 Val Asn Phe Tyr Ala Glu Asp Phe Asp Asp Ser Asn Phe Lys Ser Val
W--> 206      660      665      670
      208 aaa gta ccc ggc aac ctg gaa ctg caa ggc ttt ggc cag ccc cag tat 2185
      209 Lys Val Pro Gly Asn Leu Glu Leu Gln Gly Phe Gly Gln Pro Gln Tyr
W--> 210      675      680      685
      212 gtc aac gtc caa tat cca tgg gac ggc agt gag gag att ttc ccg ccc 2233
      213 Val Asn Val Gln Tyr Pro Trp Asp Gly Ser Glu Glu Ile Phe Pro Pro
W--> 214      690      695      700
      216 caa att cca agc aaa aat ccg ctc gct tct tat gtc aga tac ttt gac 2281
      217 Gln Ile Pro Ser Lys Asn Pro Leu Ala Ser Tyr Val Arg Tyr Phe Asp
W--> 218      705      710      715
      220 ctg gat gaa gct ttc tgg gac aag gaa gtc agc ttg aag ttt gac ggg 2329
      221 Leu Asp Glu Ala Phe Trp Asp Lys Glu Val Ser Leu Lys Phe Asp Gly
W--> 222 720      725      730      735
      224 gcg gca aca gcc atc tat gtc tgg ctg aac ggc cac ttc gtc ggc tac 2377
      225 Ala Ala Thr Ala Ile Tyr Val Trp Leu Asn Gly His Phe Val Gly Tyr
W--> 226      740      745      750
      228 ggg gaa gac tcc ttt acc cca agc gag ttt atg gtt acc aag ttc ctc 2425
      229 Gly Glu Asp Ser Phe Thr Pro Ser Glu Phe Met Val Thr Lys Phe Leu
W--> 230      755      760      765
      232 aag aaa gaa aat aac cgc ctg gca gtg gct ctc tac aag tat tct tcc 2473
      233 Lys Lys Glu Asn Asn Arg Leu Ala Val Ala Leu Tyr Lys Tyr Ser Ser
W--> 234      770      775      780
      236 gcc tcc tgg ctg gaa gac cag gac ttc tgg cgc atg tct ggt ttg ttc 2521
      237 Ala Ser Trp Leu Glu Asp Gln Asp Phe Trp Arg Met Ser Gly Leu Phe
W--> 238      785      790      795
      240 aga tca gtg act ctt cag gcc aag ccg cgt ctg cac ttg gag gac ctt 2569
      241 Arg Ser Val Thr Leu Gln Ala Lys Pro Arg Leu His Leu Glu Asp Leu
W--> 242 800      805      810      815
      244 aag ctt acg gcc agc ttg acc gat aac tac caa aaa gga aag ctg gaa 2617
      245 Lys Leu Thr Ala Ser Leu Thr Asp Asn Tyr Gln Lys Gly Lys Leu Glu
W--> 246      820      825      830
      248 gtc gaa gcc aat att gcc tac cgc ttg cca aat gcc agc ttt aag ctg 2665
      249 Val Glu Ala Asn Ile Ala Tyr Arg Leu Pro Asn Ala Ser Phe Lys Leu
W--> 250      835      840      845
      252 gaa gtg cgg gat agt gaa ggt gac ttg gtt gct gaa aag ctg ggc cca 2713
      253 Glu Val Arg Asp Ser Glu Gly Asp Leu Val Ala Glu Lys Leu Gly Pro
W--> 254      850      855      860
      256 atc aga agc gag cag ctg gaa ttc act ctg gct gat ttg cca gta gct 2761
      257 Ile Arg Ser Glu Gln Leu Glu Phe Thr Leu Ala Asp Leu Pro Val Ala
W--> 258      865      870      875
      260 gcc tgg agc gcg gaa aag cct aac ctt tac cag gtc cgc ctg tat tta 2809
      261 Ala Trp Ser Ala Glu Lys Pro Asn Leu Tyr Gln Val Arg Leu Tyr Leu
W--> 262 880      885      890      895

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## RAW SEQUENCE LISTING

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:16

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

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264 tac cag gca ggc agc ctc tta gag gtt agc cgg cag gaa gtg ggt ttc 2857
265 Tyr Gln Ala Gly Ser Leu Leu Glu Val Ser Arg Gln Glu Val Gly Phe
W--> 266          900          905          910
268 cgc aac ttt gaa cta aaa gac ggg att atg tac ctt aac ggc cag cgg 2905
269 Arg Asn Phe Glu Leu Lys Asp Gly Ile Met Tyr Leu Asn Gly Gln Arg
W--> 270          915          920          925
272 atc gtc ttc aag ggg gcc aac cgg cac gaa ttt gac agt aag ttg ggc 2953
273 Ile Val Phe Lys Gly Ala Asn Arg His Glu Phe Asp Ser Lys Leu Gly
W--> 274          930          935          940
276 cgg gct atc aca gaa gag gat atg atc tgg gat atc aag acc atg aag 3001
277 Arg Ala Ile Thr Glu Glu Asp Met Ile Trp Asp Ile Lys Thr Met Lys
W--> 278          945          950          955
280 cga agc aac atc aat gct gtc cgc tgc tct cac tac ccg aac cag tcc 3049
281 Arg Ser Asn Ile Asn Ala Val Arg Cys Ser His Tyr Pro Asn Gln Ser
W--> 282 960          965          970          975
284 ctc ttt tac cgg ctc tgt gac aag tac ggc ctt tac gtc att gat gaa 3097
285 Leu Phe Tyr Arg Leu Cys Asp Lys Tyr Gly Leu Tyr Val Ile Asp Glu
W--> 286          980          985          990
288 gct aac ctg gaa agc cac ggc acc tgg gaa aaa gtg ggg ggc cac gaa 3145
289 Ala Asn Leu Glu Ser His Gly Thr Trp Glu Lys Val Gly His Glu
W--> 290          995          1000          1005
292 gat cct agc ttc aat gtt cca ggc gat gac cag cat tgg ctg gga gcc 3193
293 Asp Pro Ser Phe Asn Val Pro Gly Asp Asp Gln His Trp Leu Gly Ala
W--> 294          1010          1015          1020
296 agc tta tcc cgg gtg aag aac atg atg gct cgg gac aag aac cat gct 3241
297 Ser Leu Ser Arg Val Lys Asn Met Met Ala Arg Asp Lys Asn His Ala
W--> 298          1025          1030          1035
300 tca atc ctg atc tgg tct tta ggc aat gag tct tac gcc ggc act gtc 3289
301 Ser Ile Leu Ile Trp Ser Leu Gly Asn Glu Ser Tyr Ala Gly Thr Val
W--> 302 1040          1045          1050          1055
304 ttt gcc caa atg gct gat tac gtc cgg aag gct gat ccg acc cgg gtt 3337
305 Phe Ala Gln Met Ala Asp Tyr Val Arg Lys Ala Asp Pro Thr Arg Val
W--> 306          1060          1065          1070
308 cag cac tat gaa ggg gtg acc cac aac cgg aag ttt gac gac gcc acc 3385
309 Gln His Tyr Glu Gly Val Thr His Asn Arg Lys Phe Asp Asp Ala Thr
W--> 310          1075          1080          1085
312 cag att gaa agc cgg atg tat gct ccg gcc aag gta att gaa gaa tac 3433
313 Gln Ile Glu Ser Arg Met Tyr Ala Pro Ala Lys Val Ile Glu Glu Tyr
W--> 314          1090          1095          1100
316 ttg acc aat aaa cca gcc aag cca ttt atc tca gtt gaa tac gct cac 3481
317 Leu Thr Asn Lys Pro Ala Lys Pro Phe Ile Ser Val Glu Tyr Ala His
W--> 318          1105          1110          1115
320 gcc atg ggc aac tcc gtc ggt gac ctg gcc gcc tac acg gcc ctg gaa 3529
321 Ala Met Gly Asn Ser Val Gly Asp Leu Ala Ala Tyr Thr Ala Leu Glu
W--> 322 1120          1125          1130          1135
324 aaa tac ccc cac tac cag ggc ggc ttc atc tgg gac tgg att gac caa 3577
325 Lys Tyr Pro His Tyr Gln Gly Gly Phe Ile Trp Asp Trp Ile Asp Gln
W--> 326          1140          1145          1150
328 gga ctg gaa aaa gac ggg cac ctg ctt tat ggg ggc gac ttc gat gac 3625

```

## VERIFICATION SUMMARY

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:17

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number  
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
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L:274 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:278 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
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L:294 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:298 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:302 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:306 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:310 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
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L:326 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
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L:358 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:362 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:366 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY

DATE: 04/16/2001

PATENT APPLICATION: US/09/700,687

TIME: 13:23:17

Input Set : A:\Cpg.pto

Output Set: N:\CRF3\04162001\I700687.raw

L:370 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:374 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:378 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:382 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1